

ANNOTATED FIG. 1

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix gap open: gap extension:
 x_dropoff: expect: wordsize: Filter:

Sequence 1 lcl|seq_1 Length 510 (1 .. 510)

Sequence 2 lcl|seq_2 Length 512 (1 .. 512)

2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0
 Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

Query: 1	MFIESFRVESPHVRYGAAEIESDYQYDITTELVHESHDGASRWIVRPKSVRYNFRTTTVP	SEQ ID 2
60	MFIESFRVESPHVRYGAAEIES+YTYDITTELVHESHDGASRW+VRPKSV+Y+FRT+ITVP	
Sbjct: 1	MFIESFRVESPHVRYGAAEIESEYRYDITTELVHESHDGASRWVVRPKSVQYHFRSTTTVP	SEQ ID 3
60	MFIESFRVESPHVRYGAAEIESEYRYDITTELVHESHDGASRWVVRPKSVQYHFRSTTTVP	
Query: 61	KLGVMLVGGNNNGSTLTAGVIANREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	SEQ ID 2
120	KLGVMLVGGNNNGSTLTAGVIA+REGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	
Sbjct: 61	KLGVMLVGGNNNGSTLTAGVIASREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	SEQ ID 3
120	KLGVMLVGGNNNGSTLTAGVIASREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	
Query: 121	IYAPFKSLLPMVNPDOLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPMES-----	SEQ ID 2
173	IYAPFKSLLPMVNPDOLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPMES-----	
Sbjct: 121	IYAPFKSLLPMVNEDDLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPMESWLAS	SEQ ID 3
180	IYAPFKSLLPMVNEDDLVFGGWDISNMNLADAMTRAKVLDIDLQKQLRPMESWLAS	
Query: 174	MVPL--PGIYDPDVIAANQGSRANNVIKGTKKEQMEQIIKDIREFKEKSKVVKVVVINTA	SEQ ID 2
231	M+P - P DP A SR ++ + + KDIREFKE IK+DK VVINTA	
Sbjct: 181	MPTSSPLTRDP---ARTMSSRE-----PRRSRGRSSKDIREFKENNMDKAVVINTA	SEQ ID 3
231	MPTSSPLTRDP---ARTMSSRE-----PRRSRGRSSKDIREFKENNMDKAVVINTA	

Fig: 1

Query: 232 NTERYSN-VCVGLNDTMENLLASVDKNEAEISPSTLYAIACV-MNGIPFIIIGSPQNTFVP SEQ ID 2
 289
 NTERYN+TICIGL T ASVDINAEISPSTLY IEG+ I G+ + P
 Sbjct: 232 NTERYNNCCLCLGLM-TNGKPSASVDRNQAEISPSTLYCHCLASLEGVRISITGALKKSWP SEQ ID 3
 290
 Query: 290 GLIDLAIKNCLI-GGDDFKSGQTIMKSVLVDFLVGAGIKPTSIVSYNHLGNNDGMNSA SEQ ID 2
 348
 G+ DLAIK GG K G+ K K+ LVDFL+GAGIKPTSIVSYNHLGNNDGMNSA
 Sbjct: 291 GIDDLAIKKKLDPGGLIQQKRGKPKKKTGLVDFLMGAGIKPTSIVSYNHLGNNDGMNSA SEQ ID 3
 350
 Query: 349 PQTFRSKEISKSNNVVDDMVSSNAILYELGEHDPDHVVVIKYVYVGDSKRAMDEYTSEIFM SEQ ID 2
 408
 PQTFRSKEISKS+VVDDMVSSNAILYE GEHPDHVVVIKYVYVGDSKRAMDEYTSEIFM
 Sbjct: 351 PQTFRSKEISKSSVVDDMVSSNAILYEPGEHDPDHVVVIKYVYVGDSKRAMDEYTSEIFM SEQ ID 3
 410
 Query: 409 GGKSTIVLHNTCEDSLLAAPIIILDVLVLLAELSTRIQLKAEGEEEKFHFSFHPVATILSYLT SEQ ID 2
 468
 GGK+TIVLHNTCEDSLLAAPIIILDVLVLLAELSTRIQLK EGEEEKFHFSFHPVATILSYLT
 Sbjct: 411 GGKNTIVLHNTCEDSLLAAPIIILDVLVLLAELSTRIQLKGEGEEKFHFSFHPVATILSYLT SEQ ID 3
 470
 Query: 469 APIVPPGTPVNVNALAKQRAMLENIMRACVGLAPENNMLEYK 510.
 APIVPPGTPVNVNALAKQRAMLENIMRACVGLAPENNMLEYK
 Sbjct: 471 APIVPPGTPVNVNALAKQRAMLENIMRACVGLAPENNMLEYK 512
 CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total
 secs.

Gapped
 Lambda K H
 0.316 0.134 0.385

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 2125
 Number of Sequences: 0
 Number of extensions: 153
 Number of successful extensions: 5
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 510
 length of database: 233,319,389
 effective HSP length: 125
 effective length of query: 385
 effective length of database: 176,133,389
 effective search space: 67811354765
 effective search space used: 67811354765

Fig:1 (Cont'd)